

**AMENDMENTS TO THE SPECIFICATION**

Please replace the paragraph at page 30, lines 3-24, with the following replacement paragraph.

In a preferred embodiment, the first functional subunit of the chimeric polypeptide of the invention comprises an F-box or portion thereof sufficient for interaction with at least one other E3 component. In an exemplary embodiment, the first functional subunit comprises at least the F-box from the human protein h- $\beta$ TrCP (corresponding to the polypeptide of SEQ ID NO: 4 which is encoded by the nucleic acid of SEQ ID No. 3), or homolog thereof or a portion thereof. This human protein is further described in Margottin et al. (1998) *Mol. Cell* 1: 565 and can be found in GenBank (Accession No. Y14153). The F-box of this protein corresponds to amino acid 148-192 (SEQ ID NO: 49, which is encoded by SEQ ID NO: 48) of the sequence shown in Margottin et al., supra, or SEQ ID No. 4. Another preferred first functional subunit comprises a polypeptide or homolog or portion thereof selected from the group consisting of Cdc4p, Grr1p, and Met30p. Yet other F-box containing proteins of which the F-box can be included in a chimeric polypeptide of the invention include Cyclin F; Skp2p; Pop1; C02F5.7; F48E8.7; MD6; YJL149w; N0376; 9934.4; 8039.5; N1161; SconB; Scon-2; fim; UFO; C02F5.7; C14B1.3; C17C3.6; C26E6.5; F43C9/1; F48E8.7; K10B2.1; T01E8.4; ZK328.7; Ro3D7; MD6; p110SIII; E3012.9K; and  $\beta$ -TrCP (see, e.g., Margottin et al., supra; Bai et al. (1996) *Cell* 86:263; Kominami et al. (1997), *Genes Dev.* 11: 1548; Li et al. (1997) *EMBO J.* 16:5629). The amino acid sequence of WD repeats of the *S. cerevisiae* Met30p, *Neurospora crassa* Scon2p and the *Xenopus levi* proteins can be found in Margollis et al., supra. Yet other F-box proteins from which portions can be used in the invention include any of the F-box containing proteins described in Bai et al., supra, or F-box containing proteins that have not been isolated yet. Such proteins can be isolated based on the sequence homology between the F-boxes, using methods known in the art and further described herein, e.g., PCR. An alignment of the F-boxes indicates the position of conserved residues (see, e.g., Bai et al., supra).